

SEQUENCE LISTING

<110> Cahoon, Rebecca E.
 Falco, Saverio C.
 Kinney, Anthony J.
 Miao, Guo-Hua

<120> Plant Polyphenol Oxidase Homologs

<130> BB1330

<140> 09/889,463

<141> 2001-07-16

<150> 60/119,590

<151> 1999-02-10

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<211> 512

<212> DNA

<213> Zea mays

<220>

<221> unsure

<222> (489)

<223> n = a, c, g or t

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<221> unsure

<222> (510)

<223> n = a, c, g or t

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gtgcgcatct cccagaggcg aacgctccga gccagacgcc caaaagcacg accgccgcga 180
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tccggtgagc gccaacgtgc tgacgtgctg cccgccgccc tcgagcgcgc tgcccgtgga 360
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<211> 150

<212> PRT

<213> Zea mays

<400> 2

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Met Ala Ser Ile Ser His Leu Ile Ala Lys Pro Ala Pro Ala Ala Thr
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Phe Pro Leu Ser Leu Pro Arg Thr Ser Ser Gly Phe Arg Pro Arg Arg
          20                      25                      30
  
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Val Thr Val Gln Arg Val Ser Cys Ala Ser Pro Arg Gly Glu Arg Ser
  
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35	40	45
Glu Pro Asp Ala Gln Lys His Asp Arg Arg Asp Val Leu Leu Gly Leu		
50	55	60
Gly Ala Leu Gly Ala Ser Ala Thr Ala Thr Leu Ala Ser Ala Arg Arg		
65	70	75 80
Ala Gly Ala Asp Pro Val Ala Thr Pro Asp Ile Ser Ser Cys Gly Gln		
85	90	95
Ala Asn Leu Pro Val Ser Ala Asn Val Leu Thr Cys Cys Pro Pro Pro		
100	105	110
Ser Ser Ala Leu Pro Val Asp Phe Ile Leu Pro Asp Ala Thr Ser Leu		
115	120	125
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130	135	140
Ala Lys Val Gln Arg Arg		
145	150	

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ccgcgcgcgc	cgccggcgcc	gaccccgctc	ccacgcccga	catctcttcc	tgccggccaag	300
cgaaccttcc	ggtagcgcc	aacgtgctga	cgtgctgccc	gccgccctcg	agcgcgctgc	360
ccgtggactt	catcctcccc	gacgccacgt	ccttgccgct	ccggacgcgc	cccgccgcgc	420
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tcccggcgga	cgaccgcgt	agcttcgcgg	cgcaggcgag	cgtgcactgc	gcctactgcg	540
acgggtcgta	cagccccgag	gggttccccg	gtgtggagct	ccagggtcac	aactcgtggc	600
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 <211> 278
 <212> PRT
 <213> Zea mays

<400> 4

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35					40					45						
Glu	Pro	Asp	Ala	Gln	Lys	His	Asp	Arg	Arg	Asp	Val	Leu	Leu	Gly	Leu	
50					55					60						
Gly	Ala	Leu	Gly	Ala	Ser	Ala	Thr	Ala	Thr	Leu	Ala	Ser	Ala	Arg	Arg	
65					70					75					80	
Ala	Gly	Ala	Asp	Pro	Val	Ala	Thr	Pro	Asp	Ile	Ser	Ser	Cys	Gly	Gln	
85					90					95						
Ala	Asn	Leu	Pro	Val	Ser	Ala	Asn	Val	Leu	Thr	Cys	Cys	Pro	Pro	Pro	
100					105					110						
Ser	Ser	Ala	Leu	Pro	Val	Asp	Phe	Ile	Leu	Pro	Asp	Ala	Thr	Ser	Leu	
115					120					125						
Pro	Leu	Arg	Thr	Arg	Pro	Ala	Ala	His	Ser	Val	Thr	Thr	Asp	Tyr	Val	
130					135					140						
Ala	Lys	Phe	Asn	Ala	Gly	Ile	Ala	Ala	Met	Lys	Ala	Leu	Pro	Ala	Asp	
145					150					155					160	
Asp	Pro	Arg	Ser	Phe	Ala	Ala	Gln	Ala	Ser	Val	His	Cys	Ala	Tyr	Cys	
165					170					175						
Asp	Gly	Ser	Tyr	Ser	Pro	Glu	Gly	Phe	Pro	Gly	Val	Glu	Leu	Gln	Val	
180					185					190						
His	Asn	Ser	Trp	Leu	Phe	Phe	Pro	Phe	His	Arg	Cys	Tyr	Leu	Tyr	Phe	
195					200					205						
Phe	Glu	Arg	Ile	Leu	Gly	Ser	Leu	Ile	Gly	Asp	Pro	Gly	Phe	Ala	Val	
210					215					220						
Pro	Phe	Trp	Asn	Trp	Asp	Ala	Pro	Asp	Gly	Met	Arg	Met	Pro	Ala	Met	
225					230					235					240	
Tyr	Ala	Asp	Arg	Ser	Ser	Gln	Leu	Phe	Asp	Pro	Arg	Arg	Asp	Ser	Arg	
245					250					255						
His	Ala	Pro	Pro	Lys	Leu	Ile	Asn	Leu	Asp	Tyr	Asn	Ala	Asn	Val	Arg	
260					265					270						
Glu	Pro	Arg	Phe	Thr	Tyr											
275																

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 <223> n = a, c, g or t

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ccgctgccct gggctacgcc taccaggacg tcgccctgcc gtggctgaac gccaagccgg 180
ccaaggaggg cgggtctccg gcgcccaccg cgggcgcgct cccggcgaca ctgaaccaga 240
ccgtgcgggg ggccgtgacg cggcccaaga cctcgaggac ccgcaaggag aaggacgcca 300
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<210> 6

<211> 126

<212> PRT

<213> Zea mays

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<221> UNSURE

<222> (117)

<223> Xaa = any amino acid

<220>

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<222> (120)

<223> Xaa = any amino acid

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 1          5          10          15
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Asp Ala Ser Phe Leu Phe Tyr Asp Glu Glu Ala Arg Leu Val Arg Val
          20          25          30
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```
Arg Val Arg Asp Cys Leu Asp Thr Ala Ala Leu Gly Tyr Ala Tyr Gln
          35          40          45
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```
Asp Val Ala Leu Pro Trp Leu Asn Ala Lys Pro Ala Lys Glu Ala Gly
          50          55          60
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Ser Pro Ala Pro Thr Ala Gly Ala Leu Pro Ala Thr Leu Asn Gln Thr
          65          70          75          80
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```
Val Arg Val Ala Val Thr Arg Pro Lys Thr Ser Arg Thr Arg Lys Glu
          85          90          95
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Lys Asp Ala Lys Glu Glu Val Leu Val Val Gln Gly Ile Glu Ile Ala
100 105 110

Asp His Ser Asn Xaa Phe Val Xaa Phe Asp Leu Phe Val Asn
115 120 125

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<212> DNA
<213> Glycine max

<220>
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cgtgtctgca gtgtataatg ttccttccaa gtctaccact ctcccttctt ccctgcatcc 180
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gaggaacatt ctacttgGCC taggagggct ttgtggtgct gctactctta acaacaaccc 360
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<213> Glycine max

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Pro Ser Ser Leu His Pro Phe Ser Gln Ser Gln Ser Thr Lys Tyr Arg
20 25 30

Lys Ser Lys His His His Thr Pro Arg Val Thr Cys Asn Ser Gly Asn
35 40 45

Gln	Asn	Lys	Gly	Glu	Lys	Pro	Asp	Ile	His	Ile	Glu	Gln	Arg	Arg	Asn
50						55					60				
Ile	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Cys	Gly	Ala	Ala	Thr	Leu	Asn	Asn
65					70					75				80	
Asn	Pro	Phe	Ala	Phe	Ala	Ala	Pro	Ile	Ser	Pro	Pro	Arg	Pro	Asn	Thr
				85					90					95	
Cys	Gly	Pro	Pro	Asp	Leu	Pro	Glu	Gly	Ala	Glu	Pro	Thr	Asn	Cys	Cys
			100					105					110		
Pro	Pro	Phe	Ser	Ser	Thr	Ile	Ile	Asp	Phe	Lys	Phe	Pro	Pro	Ser	Asn
		115					120					125			
Lys	Pro	Leu	Arg	Val	Arg	Pro	Ala	Ala	His	Leu	Val	Asp	Lys	Asn	Tyr
	130					135					140				
Leu	Ala	Lys	Tyr	Lys	Lys	Ala	Ile	Xaa	Leu	Met	Lys				
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<210> 9
 <211> 2485
 <212> DNA
 <213> Glycine max

<400> 9

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ctagagtgc	atgtaatagt	ggaaaccaa	acaaaggaga	aaaaccagat	attcatatag	300
aacaaaggag	gaacattcta	cttggcctag	gagggctttg	tgggtgctgt	actcttaaca	360
acaacccttt	tgcatttgct	gcgccaatat	ctcctccaga	cctaaccaca	tgtggtccac	420
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atgatgatag	tgttggtgtg	acgttggttc	cgaggtatgg	gaaagggcgt	gtccaaattg	1860
gaggcatcaa	gatagatctt	gttgcagatt	aaaaaatatt	tatatacttc	gactgtttta	1920
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acaatccccc tccaaaaaaa tttgccacc caaaagggaa aaggagaccc cccctgtagc 2340
ggcaaaaaaa ccgggggggg tgtgggggat acccaaatgt aaccgaaaaa tttgaaaacc 2400
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<210> 10
<211> 601
<212> PRT
<213> Glycine max

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Ala Val Tyr Asn Val Pro Ser Lys Ser Thr Thr Leu Pro Ser Ser Leu
          20          25          30

His Pro Phe Ser Gln Ser Gln Ser Thr Lys Tyr Arg Lys Ser Lys His
          35          40          45

His His Thr Pro Arg Val Thr Cys Asn Ser Gly Asn Gln Asn Lys Gly
          50          55          60

Glu Lys Pro Asp Ile His Ile Glu Gln Arg Arg Asn Ile Leu Leu Gly
          65          70          75          80

Leu Gly Gly Leu Cys Gly Ala Ala Thr Leu Asn Asn Asn Pro Phe Ala
          85          90          95

Phe Ala Ala Pro Ile Ser Pro Pro Asp Leu Thr Thr Cys Gly Pro Pro
          100          105          110

Asp Leu Pro Glu Gly Ala Glu Pro Thr Asn Cys Cys Pro Pro Phe Ser
          115          120          125

Ser Thr Ile Ile Asp Phe Lys Phe Pro Pro Ser Asn Lys Pro Leu Arg
          130          135          140

Val Arg Pro Ala Ala His Leu Val Asp Lys Asn Tyr Leu Ala Lys Tyr
          145          150          155          160

Lys Lys Ala Ile Asp Leu Met Lys Lys Leu Pro Ala Asn Asp Pro Arg
          165          170          175

Asn Phe Met Gln Gln Ala Asn Val His Cys Ala Tyr Cys Thr Gly Ser
          180          185          190

Tyr Asp Gln Val Gly Phe Pro Gly Leu Glu Leu Gln Val His Ser Ser
          195          200          205

Trp Leu Phe Phe Pro Tyr His Arg Trp Phe Leu Tyr Phe Tyr Glu Arg
          210          215          220

Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr Phe Ala Leu Pro Phe Trp
          225          230          235          240

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Asn	Trp	Asp	Ala	Pro	Lys	Gly	Met	Gln	Leu	Pro	Ser	Ile	Tyr	Ala	Asp	
				245					250						255	
Pro	Lys	Ser	Pro	Leu	Tyr	Asp	Pro	Leu	Arg	Asn	Ala	Asn	His	Gln	Pro	
			260					265					270			
Pro	Thr	Leu	Val	Asp	Phe	Asp	Phe	Asn	Leu	Asp	Asn	Pro	Ile	Ser	Asn	
		275					280					285				
Gly	Arg	Ile	Ser	Thr	Asn	Leu	Thr	Ile	Met	Tyr	Arg	Gln	Leu	Val	Ser	
	290					295					300					
Asn	Gly	Lys	Thr	Pro	Thr	Leu	Phe	Leu	Gly	Asn	Pro	Tyr	Arg	Ala	Gly	
305					310					315					320	
Asp	Ala	Pro	Asp	Pro	Gly	Gly	Gly	Ser	Val	Glu	Gly	Val	Pro	His	Gly	
				325					330					335		
Pro	Val	His	Leu	Trp	Thr	Gly	Asp	Ile	Asn	Gln	Pro	Asn	Ile	Glu	Asn	
			340					345					350			
Met	Gly	Asp	Phe	Tyr	Ser	Ala	Ala	Arg	Asp	Pro	Ile	Phe	Tyr	Ser	His	
		355					360					365				
His	Ser	Asn	Val	Asp	Arg	Met	Trp	Ser	Ile	Trp	Lys	Thr	Leu	Gly	Gly	
	370					375					380					
Lys	Arg	Arg	Asp	Phe	Thr	Asp	Ser	Asp	Trp	Leu	Glu	Ser	Gly	Leu	Leu	
385					390					395					400	
Phe	Tyr	Asp	Glu	Asn	Lys	Asn	Leu	Val	Arg	Val	Lys	Val	Lys	Asp	Cys	
				405					410					415		
Leu	Asp	Thr	Arg	Lys	Leu	Gly	Tyr	Val	Tyr	Gln	Asp	Val	Glu	Ile	Pro	
			420					425					430			
Trp	Leu	Lys	Ser	Lys	Pro	Ser	Pro	Arg	Arg	Ser	Arg	Val	Gln	Lys	Val	
		435					440					445				
Ala	Leu	Gly	Pro	His	Phe	Asn	Thr	Gly	Val	Ala	Arg	Ala	Ala	Glu	Thr	
	450					455				460						
Ser	Arg	Asn	Val	Gln	Phe	Pro	Leu	Val	Leu	Asp	Ser	Val	Val	Ser	Ile	
465					470					475					480	
Val	Val	Lys	Arg	Pro	Lys	Lys	Ser	Arg	Ser	Lys	Lys	Glu	Lys	Glu	Glu	
				485					490					495		
Glu	Glu	Glu	Val	Leu	Val	Ile	Glu	Gly	Val	Glu	Tyr	Asp	Ser	Asn	Ile	
			500					505					510			
Pro	Val	Lys	Phe	Asp	Val	Leu	Ile	Asn	Asp	Glu	Asp	Asp	Lys	Gln	Ile	
		515					520					525				
Gln	Pro	Glu	Asp	Ser	Glu	Tyr	Ala	Gly	Ser	Phe	Val	Thr	Val	Pro	His	
	530					535					540					
Ser	His	Lys	His	Lys	Asn	Lys	Lys	Ile	Ile	Thr	Cys	Leu	Arg	Leu	Gly	
545					550					555					560	

Leu Thr Asp Leu Leu Glu Glu Leu Glu Ala Glu Asp Asp Asp Ser Val
565 570 575

Val Val Thr Leu Val Pro Arg Tyr Gly Lys Gly Arg Val Gln Ile Gly
580 585 590

Gly Ile Lys Ile Asp Leu Val Ala Asp
595 600

<210> 11
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<212> DNA
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<220>
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cgaggcagac gcggcgccctg acgtgcaagg caaccggcgg ccgcgtcgac cgccgcgacg 180
tgctcctcgg cctcggcagc gccgcggcgg ccgggctggg cgcgcagcgg ggccgagggg 240
cgattgccgc gcccatccag gcccgggacc tcggcaactg caaccgccc gacctccga 300
acacggcgcc tgacaacaac tgctgcccga cgtccggcac cggcatcatc gacttcntgt 360
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<210> 12
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<213> Triticum aestivum

<220>
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<223> Xaa = any amino acid

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Cys Lys Ala Thr Gly Gly Arg Val Asp Arg Arg Asp Val Leu Leu Gly
35 40 45
Leu Gly Ser Ala Ala Ala Ala Gly Leu Gly Ala Gln Arg Gly Arg Gly
50 55 60
Ala Ile Ala Ala Pro Ile Gln Ala Pro Asp Leu Gly Asn Cys Asn Pro
65 70 75 80
Pro Asp Leu Pro Asn Thr Ala Pro Asp Thr Asn Cys Cys Pro Thr Ser
85 90 95
Gly Thr Gly Ile Ile Asp Phe Val Leu Pro Pro Ala Pro Arg Ala Pro
100 105 110
Leu Arg Val Arg Pro Ala Ala His Leu Ala Asp Ala Glu Tyr Leu Ala
115 120 125
Lys Tyr Glu Arg Ala Val Ala Leu Met Lys Gln Leu Pro Ala Asp Asp
130 135 140
Pro Arg Ser Ser Lys Gln Gln Trp Arg Val His Cys Ala Tyr Cys Glu
145 150 155 160
Arg Pro Xaa Arg Gln Val
165

<210> 13
<211> 1993
<212> DNA
<213> Triticum aestivum

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cgaggcagac gcggcgccctg acgtgcaagg caaccggcgg ccgcgtcgac cgccgcgacg 180
tgctcctcgg cctcggcagc gccgcggcgg ccgggctggg cgcgcagcgg gcccgagggg 240
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acacggcgcc tgacaccaac tgctgcccga cgtccggcac cggcatcatc gacttcgtgc 360
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ccaacaggtc gtcgcgctc tacaacgaga ggcgcaacc cgcgccaccag ccgcgcttcc 780
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ccgtgtggtg tatatctaaa caagtcgctc atgagcgatc gttgcgtgct ttacgtcacg 1800
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1993

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<210> 14
<211> 557
<212> PRT
<213> Triticum aestivum

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<400> 14
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Leu Gln Ala Leu Val Pro Thr Lys Ala Arg Gln Thr Arg Arg Leu Thr
      20              25              30

Cys Lys Ala Thr Gly Gly Arg Val Asp Arg Arg Asp Val Leu Leu Gly
      35              40              45

Leu Gly Ser Ala Ala Ala Ala Gly Leu Gly Ala Gln Arg Ala Arg Gly
      50              55              60

Ala Ile Ala Ala Pro Ile Gln Ala Pro Asp Leu Gly Asn Cys Asn Pro
      65              70              75              80

Pro Asp Leu Pro Asn Thr Ala Pro Asp Thr Asn Cys Cys Pro Thr Ser
      85              90              95

Gly Thr Gly Ile Ile Asp Phe Val Leu Pro Pro Ala Ser Ser Ala Pro
      100              105              110

Leu Arg Val Arg Pro Ala Ala His Leu Ala Asp Ala Glu Tyr Leu Ala
      115              120              125

Lys Tyr Glu Arg Ala Val Ala Leu Met Lys Gln Leu Pro Ala Asp Asp
      130              135              140

Pro Arg Ser Phe Glu Gln Gln Trp Arg Val His Cys Ala Tyr Cys Asp
      145              150              155              160

Gly Ala Tyr Asp Gln Val Gly Phe Pro Asp Leu Glu Ile Gln Val His
      165              170              175

Asn Cys Trp Leu Phe Phe Pro Trp His Arg Phe Tyr Leu Tyr Phe His
      180              185              190

Glu Arg Ile Leu Gly Lys Leu Ile Gly Asp Asp Thr Phe Ala Leu Pro
      195              200              205

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Gly Asp Lys Thr Val Val Val Ser Leu Val Pro Arg Cys Gly Gly Glu
530 535 540

Leu Val Thr Ile Gly Gly Val Ser Ile Gly Tyr Thr Lys
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<210> 15
<211> 852
<212> DNA
<213> Glycine max

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<222> (515)
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<220>
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 <222> (848)
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 cttcttccct ttccatcggt ggtatcttta tttctatgaa aggatcttgg ggagcttgat 180
 caatgatcca acctttgccc ttccattttg gaactgggat gctcctaagg gcatgcaact 240
 tccttccatt tacgcagacc ctaaatcacc cctttatgac actctccgca atgccaatca 300
 tcaaccccca aactcgtag acctcgactt caatctcgag gatcctattt ccaatggcaa 360
 aatttccaac aacctcacca taatgtatan gcaagttgtg tctaacggga agactcctac 420
 attgttcctt ggaaatcctt accgtgctgg ggatgagcct gaccggggtt ttggatcagt 480
 agagaatggt ccacatggcc ctgttcatct ttggncgggt gatatcaacc aacctaacat 540
 tgngaacatg ggaactttct attcagctgc aggagacccc attttttatt ctcatcattc 600
 agacattgat aagatgtggt ccatatggaa aacactttgt gggaaaagaa gggattttac 660
 tgattcantt gggtaaaatc tgcgttctct tctacgatga taacaagaac cttgtgcntn 720
 tnaaggcaag gatctcntga cactanaaac taggtatggt tacaagattt gacatccatg 780
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 <211> 221
 <212> PRT
 <213> Glycine max

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 <222> (130)
 <223> Xaa = any amino acid

<220>
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 <222> (172)
 <223> Xaa = any amino acid

<220>
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 <222> (181)
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 20 25 30
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 35 40 45
 Leu Tyr Phe Tyr Glu Arg Ile Leu Gly Ser Leu Ile Asn Asp Pro Thr
 50 55 60
 Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Pro Lys Gly Met Gln Leu
 65 70 75 80
 Pro Ser Ile Tyr Ala Asp Pro Lys Ser Pro Leu Tyr Asp Thr Leu Arg
 85 90 95
 Asn Ala Asn His Gln Pro Pro Thr Leu Val Asp Leu Asp Phe Asn Leu
 100 105 110
 Glu Asp Pro Ile Ser Asn Gly Lys Ile Ser Asn Asn Leu Thr Ile Met
 115 120 125
 Tyr Xaa Gln Val Val Ser Asn Gly Lys Thr Pro Thr Leu Phe Leu Gly
 130 135 140
 Asn Pro Tyr Arg Ala Gly Asp Glu Pro Asp Pro Gly Phe Gly Ser Val
 145 150 155 160
 Glu Asn Val Pro His Gly Pro Val His Leu Trp Xaa Gly Asp Ile Asn
 165 170 175
 Gln Pro Asn Ile Xaa Asn Met Gly Thr Phe Tyr Ser Ala Ala Gly Asp
 180 185 190
 Pro Ile Phe Tyr Ser His His Ser Asp Ile Asp Lys Met Trp Ser Ile
 195 200 205
 Trp Lys Thr Leu Cys Gly Lys Arg Arg Asp Phe Thr Asp
 210 215 220

<210> 17
 <211> 522
 <212> DNA
 <213> Glycine max

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 catcatattc ctagaatcac atgcagtggg aaccaaaca atccaacacc aaaccctaata 180
 tcccaggagg aacctccaca tattgttagga cataggagga acgttctact tggccttagga 240
 gggctttgtg gtgctgttac tcttaacaac aacaaccctt ttgcctttgc agctccaata 300
 tctcctcctg acctaaacac gtgcggtcca ccagacctac ccgcaggtgt aaaacccacc 360
 aattgttgcc ccccatcttc caaaatcata gatttcaagt tctctccctc taaccaaccc 420
 ttgagggtaa gaccagccgc acatttggtc aacgatgagt atctagccaa atacaaaaaa 480
 agccttgacc tcatgaaaaa actcccctct gatgaccggg tt 522

<210> 18
 <211> 174

<212> PRT
 <213> Glycine max

<400> 18

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Ser	Ile	Ala	Pro	Pro	Ser	Pro	Leu	His	Pro	Phe	Ser	Arg	Phe	Gln	Ser
			20					25					30		
Ile	Lys	Asn	Arg	Lys	Pro	Lys	Pro	His	His	Ile	Pro	Arg	Ile	Thr	Cys
		35					40					45			
Ser	Gly	Asn	Gln	Asn	Asn	Pro	Thr	Pro	Asn	Pro	Asn	Ser	Gln	Gly	Glu
	50					55					60				
Pro	Pro	His	Ile	Val	Gly	His	Arg	Arg	Asn	Val	Leu	Leu	Gly	Leu	Gly
65					70					75					80
Gly	Leu	Cys	Gly	Ala	Val	Thr	Leu	Asn	Asn	Asn	Asn	Pro	Phe	Ala	Phe
				85					90					95	
Ala	Ala	Pro	Ile	Ser	Pro	Pro	Asp	Leu	Asn	Thr	Cys	Gly	Pro	Pro	Asp
			100					105					110		
Leu	Pro	Ala	Gly	Val	Lys	Pro	Thr	Asn	Cys	Cys	Pro	Pro	Ser	Ser	Lys
	115						120					125			
Ile	Ile	Asp	Phe	Lys	Phe	Ser	Pro	Ser	Asn	Gln	Pro	Leu	Arg	Val	Arg
	130					135					140				
Pro	Ala	Ala	His	Leu	Val	Asn	Asp	Glu	Tyr	Leu	Ala	Lys	Tyr	Lys	Lys
145					150					155					160
Ser	Leu	Asp	Leu	Met	Lys	Lys	Leu	Pro	Ser	Asp	Asp	Arg	Val		
			165						170						

<210> 19

<211> 1989

<212> DNA

<213> Glycine max

<400> 19

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aaaacccccat	catattccta	gaatcacatg	cagtggaaac	caaaacaatc	caacacccaaa	180
ccctaattcc	cagggagaaac	ctccacatat	tgtaggacat	aggaggaacg	ttctacttgg	240
cctaggaggg	ctttgtgg	ctgttactct	taacaacaac	aacccttttg	cctttgcagc	300
tccaatatct	cctcctgacc	taaacacgtg	cgggccacca	gacctaccgc	caggtgtaaa	360
acccaccaat	tgttgcccc	catcttccaa	aatcatagat	ttcaagttct	ctccctctaa	420
ccaacccttg	agggtaagac	cagccgcaca	tttgggtcaac	gatgagtatc	tagccaaata	480
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caatctcgag	gatcctat	ccaatggcaa	aatttccaac	aacctcacca	taatgtatag	900
gcaagtgtg	tctaacggga	agactcctac	attgttcctt	ggaaatcctt	accgtgctgg	960
ggatgagcct	gaccggggtt	ttggatcagt	agagaatggt	ccacatggcc	ctgttcactc	1020


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<210> 20

<211> 599

<212> PRT

<213> Glycine max

<400> 20

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Ile Ser Pro Leu Ser Phe Val Pro Thr Val Asn Asn Val Ser Ser Asn
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```

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Ser Ile Ala Pro Pro Ser Pro Leu His Pro Phe Ser Arg Phe Gln Ser
          20              25              30

```

```

Ile Lys Asn Arg Lys Pro Lys Pro His His Ile Pro Arg Ile Thr Cys
          35              40              45

```

```

Ser Gly Asn Gln Asn Asn Pro Thr Pro Asn Pro Asn Ser Gln Gly Glu
          50              55              60

```

```

Pro Pro His Ile Val Gly His Arg Arg Asn Val Leu Leu Gly Leu Gly
          65              70              75              80

```

```

Gly Leu Cys Gly Ala Val Thr Leu Asn Asn Asn Asn Pro Phe Ala Phe
          85              90              95

```

```

Ala Ala Pro Ile Ser Pro Pro Asp Leu Asn Thr Cys Gly Pro Pro Asp
          100              105              110

```

```

Leu Pro Ala Gly Val Lys Pro Thr Asn Cys Cys Pro Pro Ser Ser Lys
          115              120              125

```

```

Ile Ile Asp Phe Lys Phe Ser Pro Ser Asn Gln Pro Leu Arg Val Arg
          130              135              140

```

```

Pro Ala Ala His Leu Val Asn Asp Glu Tyr Leu Ala Lys Tyr Lys Lys
          145              150              155              160

```

```

Ala Leu Asp Leu Met Lys Lys Leu Pro Ser Asp Asp Pro Arg Asn Phe
          165              170              175

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Thr Gln Gln Ala Asn Val His Cys Ala Tyr Cys Asp Gly Ala Tyr His
          180              185              190

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Gln	Val	Gly	Phe	Pro	Asp	Leu	Asp	Leu	Gln	Val	His	Asn	Ser	Trp	Leu
		195					200					205			
Phe	Phe	Pro	Phe	His	Arg	Trp	Tyr	Leu	Tyr	Phe	Tyr	Glu	Arg	Ile	Leu
	210					215					220				
Gly	Ser	Leu	Ile	Asn	Asp	Pro	Thr	Phe	Ala	Leu	Pro	Phe	Trp	Asn	Trp
225					230					235					240
Asp	Ala	Pro	Lys	Gly	Met	Gln	Leu	Pro	Ser	Ile	Tyr	Ala	Asp	Pro	Lys
				245					250					255	
Ser	Pro	Leu	Tyr	Asp	Thr	Leu	Arg	Asn	Ala	Asn	His	Gln	Pro	Pro	Thr
			260					265					270		
Leu	Val	Asp	Leu	Asp	Phe	Asn	Leu	Glu	Asp	Pro	Ile	Ser	Asn	Gly	Lys
		275					280					285			
Ile	Ser	Asn	Asn	Leu	Thr	Ile	Met	Tyr	Arg	Gln	Val	Val	Ser	Asn	Gly
	290					295					300				
Lys	Thr	Pro	Thr	Leu	Phe	Leu	Gly	Asn	Pro	Tyr	Arg	Ala	Gly	Asp	Glu
305					310					315					320
Pro	Asp	Pro	Gly	Phe	Gly	Ser	Val	Glu	Asn	Val	Pro	His	Gly	Pro	Val
				325					330					335	
His	Leu	Trp	Thr	Gly	Asp	Ile	Asn	Gln	Pro	Asn	Ile	Glu	Asn	Met	Gly
			340					345					350		
Thr	Phe	Tyr	Ser	Ala	Ala	Arg	Asp	Pro	Ile	Phe	Tyr	Ser	His	His	Ser
		355					360					365			
Asn	Ile	Asp	Arg	Met	Trp	Ser	Ile	Trp	Lys	Thr	Leu	Gly	Gly	Lys	Arg
	370					375					380				
Arg	Asp	Phe	Thr	Asp	Ser	Asp	Trp	Leu	Glu	Ser	Ala	Phe	Leu	Phe	Tyr
385					390					395					400
Asp	Glu	Asn	Lys	Asn	Leu	Val	Arg	Val	Lys	Val	Lys	Asp	Ser	Leu	Asp
				405					410					415	
Thr	Arg	Lys	Leu	Gly	Tyr	Val	Tyr	Gln	Asp	Val	Asp	Ile	Pro	Trp	Leu
			420					425					430		
Asn	Ser	Lys	Pro	Thr	Pro	Arg	Arg	Ser	Arg	Val	Gln	Lys	Val	Ala	Leu
		435					440					445			
Ala	Gln	Asn	Phe	Gly	Val	Gly	Ala	Ala	His	Ala	Ala	Glu	Thr	Ser	Arg
						455					460				
Asn	Val	Lys	Phe	Pro	Leu	Val	Leu	Asp	Ser	Val	Val	Ser	Thr	Met	Val
465					470					475					480
Lys	Arg	Pro	Asn	Lys	Ser	Arg	Ser	Lys	Lys	Glu	Lys	Glu	Glu	Glu	Glu
				485					490					495	
Glu	Val	Leu	Val	Ile	Glu	Gly	Ile	Glu	Phe	Glu	Arg	Asn	Thr	Pro	Val
			500					505					510		

Lys Phe Asp Val Phe Ile Asn Asp Glu Asp Asp Lys Gln Ile Arg Pro
 515 520 525
 Asp Asn Thr Glu Phe Ala Gly Ser Phe Val Ser Val Pro His Ser His
 530 535 540
 Met His Lys Asn Lys Asp Ile Ile Thr Cys Leu Arg Leu Gly Leu Thr
 545 550 555 560
 Asp Leu Leu Glu Glu Leu Glu Ala Glu Asp Asp Asp Ser Val Arg Val
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 Lys Ile Glu Leu Leu Ser Asp
 595

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 <211> 887
 <212> DNA
 <213> Glycine max

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<220>
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 <222> (60)
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<220>
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 <222> (618)
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 <222> (792)
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<220>
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 <222> (854)
 <223> n = a, c, g or t

<220>
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 <222> (865)
 <223> n = a, c, g or t

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 tctacgatga gaataagaac cttgtgagag taaagggtta agattgtctt gacgagagaa 180
 aactagggta tggtttaccaa gatgtagaca ttccatgggt aaactctagg cccacaccgc 240
 gaaggtctag gggttcaaaa gttgcactag cacaaaattt tgggtgttgg gcagcacgtg 300
 ctgctgagac ttcaaggaat gtgaagttcc cactagtgtt ggattcagtt gtgagcacia 360

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gtgtgcctca ttcacatatg cacaaaaaca aggacatcat tacttgtttg aggctgggac 600
ttacggattt gttggaanga attggaagcg gaagatgatg acagtgttag ggtgacgctg 660
gttccgagat atgggaaagg gcgtgtttaa atcaagaggc atcaaaatag agcttccttc 720
ggattgaaaa ttatctatat gcttcaacta cttatatatg tgtgtgtggt aatacatata 780
tggttactaa gnttccaata aagtgtgtaa ctcataaaga gatattatgt atttcctatc 840
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<210> 22
<211> 265
<212> PRT
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<221> UNSURE
<222> (20)
<223> Xaa = any amino acid

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<220>
<221> UNSURE
<222> (263)
<223> Xaa = any amino acid

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<400> 22
Asp Pro Ile Phe Phe Ser His His Ser Asn Xaa Val Arg Met Trp Ser
 1             5             10             15

His Met Lys Xaa Leu Val Gly Lys Gly Lys Asp Phe Thr Asp Ser Asp
          20             25             30

Trp Leu Glu Ser Gly Phe Leu Phe Tyr Asp Glu Asn Lys Asn Leu Val
          35             40             45

Arg Val Lys Val Lys Asp Cys Leu Asp Glu Arg Lys Leu Gly Tyr Val
          50             55             60

Tyr Gln Asp Val Asp Ile Pro Trp Leu Asn Ser Arg Pro Thr Pro Arg
 65             70             75             80

Arg Ser Arg Val Gln Lys Val Ala Leu Ala Gln Asn Phe Gly Val Gly
          85             90             95

Ala Ala Arg Ala Ala Glu Thr Ser Arg Asn Val Lys Phe Pro Leu Val
          100            105            110

Leu Asp Ser Val Val Ser Thr Met Val Lys Arg Pro Asn Lys Ser Arg
          115            120            125

Ser Lys Lys Glu Lys Glu Glu Glu Glu Glu Val Leu Val Ile Glu Gly
          130            135            140

Ile Glu Phe Glu Arg Asn Thr Pro Val Lys Phe Asp Val Phe Ile Asn
          145            150            155            160

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Asp Glu Asp Asp Lys Gln Ile Arg Pro Asp Asn Thr Glu Phe Ala Gly
 165 170 175
 Ser Phe Val Ser Val Pro His Ser His Met His Lys Asn Lys Asp Ile
 180 185 190
 Ile Thr Cys Leu Arg Leu Gly Leu Thr Asp Leu Leu Glu Glu Leu Glu
 195 200 205
 Ala Glu Asp Asp Asp Ser Val Arg Val Thr Leu Val Pro Arg Tyr Gly
 210 215 220
 Lys Gly Arg Val Lys Ile Lys Arg His Gln Asn Arg Ala Ser Phe Gly
 225 230 235 240
 Leu Lys Ile Ile Tyr Met Leu Gln Leu Leu Ile Tyr Val Cys Val Val
 245 250 255
 Ile His Ile Trp Leu Leu Xaa Phe Gln
 260 265

<210> 23
 <211> 510
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (478)
 <223> n = a, c, g or t

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 atcacattcc tagaaccaca tgcagtga aaacaaacaa tccaacacca aacccatccg 180
 aaggagaact atcacatatt gtaggacata ggaggaatgt tctacttggc ctaggagggc 240
 tttgtggtgc agttactctt aacaacaacc cttttgcctt tgcagctcca atatctcttc 300
 cagacctaaa cacacatgtg gtccaccaga cacaccgcg ggtgcaaadc ccaccaattt 360
 gttgcccccc atcttccaaa aatcatagat ttcaaagggt cctccttctt aaaccaaccc 420
 cttgagggta agaccaagcg ggcacatttg ggtcaaaccg atgaaataat ctaagccnaa 480
 aatacaaaaa aaggcccttt gacctcaatg 510

<210> 24
 <211> 138
 <212> PRT
 <213> Glycine max

<400> 24
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 20 25 30
 Lys Asn Arg Lys Pro Lys Arg His His Ile Pro Arg Thr Thr Cys Ser
 35 40 45
 Glu Asn Gln Asn Asn Pro Thr Pro Asn Pro Ser Glu Gly Glu Leu Ser
 50 55 60

His Ile Val Gly His Arg Arg Asn Val Leu Leu Gly Leu Gly Gly Leu
 65 70 75 80
 Cys Gly Ala Val Thr Leu Asn Asn Asn Pro Phe Ala Phe Ala Ala Pro
 85 90 95
 Ile Ser Pro Pro Asp Leu Asn Thr His Val Val His Gln Thr His Pro
 100 105 110
 Arg Val Gln Ile Pro Pro Ile Cys Cys Pro Pro Ser Ser Lys Asn His
 115 120 125
 Arg Phe Gln Arg Phe Pro Pro Ser Lys Pro
 130 135

<210> 25
 <211> 988
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (962)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (970)..(971)
 <223> n = a, c, g or t

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 ccatcatcat attcctagag tgacatgcag tgacaaccaa aaaccaaaaca catctggaga 180
 actagtactc ccacatagga ggaacattct acttggccta ggagggcttt gtggtgctgc 240
 tgctactctt aacaacatcc cttttgccaa tgctgcccc aactttggtc cagacctaac 300
 cacatgtgtt caagcagaac taccggaagg tgtagaacc accaattgtt gtcccccaat 360
 ttccacaaac atcatagatt tcaagttccc tccctccaac caacccttgc gtgtacgatc 420
 cgctgctcat ctggtcaaca aagactatct agctaaatac gagaaagccg ttaacctgat 480
 gaaaaatctc ccgtcagatg atccacgtag tttcgcgcaa caagccaaag ttcattgtgc 540
 ttattgcgac ggtggatata accaactagg ctccctgac ctgatatcg aagtgcactt 600
 ctcttggtc ttctttcctt accacagatg gtatctctat ttccatgaaa ggatattggc 660
 gagcttgatc aatgatccaa cctttgctct tccattttgg aactgggatg ctctggggg 720
 catgcaactt cttccatgt acgcagatcc caaatcacc ctttatgatt ctctacgcaa 780
 tgccaacat caaccaccaa cacttgtaaa ccttgacttt actatcgagg atcctaattgc 840
 agaggcaa atctccacca acctcaccac aatgtatagg caagcttggtg tctaacgcaa 900
 agactccaac attgttcttc ggaaatcctt atcgtgctgg ggatcagcta accctgggtg 960
 gnggtccgtn nagagcactc cacatggg 988

<210> 26
 <211> 274
 <212> PRT
 <213> Glycine max

<400> 26
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 1 5 10 15

Ser Asn Ser Pro Ser Ser Leu His His Pro Phe Ser Gln Ile Gln Ser

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Ala	Lys	Tyr	Arg	Lys	Pro	Lys	Arg	His	His	His	Ile	Pro	Arg	Val	Thr	
35					40					45						
Cys	Ser	Asp	Asn	Gln	Lys	Pro	Asn	Thr	Ser	Gly	Glu	Leu	Val	Leu	Pro	
50					55					60						
His	Arg	Arg	Asn	Ile	Leu	Leu	Gly	Leu	Gly	Gly	Leu	Cys	Gly	Ala	Ala	
65					70					75					80	
Ala	Thr	Leu	Asn	Asn	Ile	Pro	Phe	Ala	Asn	Ala	Ala	Pro	Ile	Leu	Gly	
85					90					95						
Pro	Asp	Leu	Thr	Thr	Cys	Val	Gln	Ala	Glu	Leu	Pro	Glu	Gly	Val	Glu	
100					105					110						
Pro	Thr	Asn	Cys	Cys	Pro	Pro	Ile	Ser	Thr	Asn	Ile	Ile	Asp	Phe	Lys	
115					120					125						
Phe	Pro	Pro	Ser	Asn	Gln	Pro	Leu	Arg	Val	Arg	Ser	Ala	Ala	His	Leu	
130					135					140						
Val	Asn	Lys	Asp	Tyr	Leu	Ala	Lys	Tyr	Glu	Lys	Ala	Val	Asn	Leu	Met	
145					150					155					160	
Lys	Asn	Leu	Pro	Ser	Asp	Asp	Pro	Arg	Ser	Phe	Ala	Gln	Gln	Ala	Lys	
165					170					175						
Val	His	Cys	Ala	Tyr	Cys	Asp	Gly	Gly	Tyr	His	Gln	Leu	Gly	Phe	Pro	
180					185					190						
Asp	Leu	Asp	Leu	Glu	Val	His	Phe	Ser	Trp	Leu	Phe	Phe	Pro	Tyr	His	
195					200					205						
Arg	Trp	Tyr	Leu	Tyr	Phe	His	Glu	Arg	Ile	Leu	Ala	Ser	Leu	Ile	Asn	
210					215					220						
Asp	Pro	Thr	Phe	Ala	Leu	Pro	Phe	Trp	Asn	Trp	Asp	Ala	Pro	Gly	Gly	
225					230					235					240	
Met	Gln	Leu	Pro	Ser	Met	Tyr	Ala	Asp	Pro	Lys	Ser	Pro	Leu	Tyr	Asp	
245					250					255						
Ser	Leu	Arg	Asn	Ala	Asn	His	Gln	Pro	Pro	Thr	Leu	Val	Asn	Leu	Asp	
260					265					270						

Phe Thr

<210> 27
 <211> 2044
 <212> DNA
 <213> Glycine max

<400> 27
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 attccccttc ttccttgcat catccctttt cacaaattca atccgctaaa tatcgaaaac 120
 caaaacgcc aatcatatatt cctagagtga catgcagtga caaccaaaaa ccaaacacat 180
 ctggagaact agtactccca cataggagga acattctact tggcctagga gggctttgtg 240

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gtgctgctgc tactotttaac aacatccctt ttgccaatgc tgccccaata cttggtccag 300
acctaaccac atgtgttcaa gcagaactac ccgaagggtg agaaccacc aattgtgtgc 360
ccccaatbbc cacaacatc atagatttca agttccctcc ctccaacca cccttgcgtg 420
tacgatccgc tgctcatctg gtcaacaaag actatctagc taaatacgag aaagccgtta 480
acctgatgaa aaatctcccg tcagatgac cactagttt cgcgcaacaa gccaaagttc 540
attgtgctta ttgcgacggt ggatatcacc aactaggctt ccctgacctt gatctcgaag 600
tgcacttctc ttggctcttc tttccttacc acagatggta tctctatttc catgaaagga 660
tattggcgag cttgatcaat gatccaacct ttgctcttcc attttggaac tgggatgctc 720
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acgcaaagac tccaacattg ttcttcggaa atccttatcg tgctggggat cagcctaacc 960
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ataagaacct tgtgctgtg aagactaagg attgtcttga cacgagaaag ttagggatatg 1260
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aagggtattg gtttgagagc agcacagggt tgaagtttga tgtgtttatt aatgatgaag 1560
atgataagtt ggtcaagcca gataatacgg agtttgcagg aagctttgtg agtgtgcctc 1620
attcgcata gcatcacaaa aacaacaaga agattgttac ttgtttgagg ttgggactaa 1680
cggatttgtt ggaagaattg ggagcagaag atgatgatag tgttctagta acattgggtc 1740
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gaaattaaat tgtttatata cttcaaatgt gtgtttgtgc tgtaggtagt aatgcacgca 1860
tggttccttg aagaatttca aatgacgcag gtcactcaga cggagatata tatagtgtat 1920
ttcctataat ataagtttga gacatgtatt agaataatat agcatatcct tattatccta 1980
tggtcactta ctgtgaaata aaataatatt gttgtgatat aaaaaaaaaa aaaaaaaaaa 2040
aaaa 2044

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<210> 28
 <211> 599
 <212> PRT
 <213> Glycine max

<400> 28
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 20 25 30
 Gln Ser Ala Lys Tyr Arg Lys Pro Lys Arg His His His Ile Pro Arg
 35 40 45
 Val Thr Cys Ser Asp Asn Gln Lys Pro Asn Thr Ser Gly Glu Leu Val
 50 55 60
 Leu Pro His Arg Arg Asn Ile Leu Leu Gly Leu Gly Gly Leu Cys Gly
 65 70 75 80
 Ala Ala Ala Thr Leu Asn Asn Ile Pro Phe Ala Asn Ala Ala Pro Ile
 85 90 95
 Leu Gly Pro Asp Leu Thr Thr Cys Val Gln Ala Glu Leu Pro Glu Gly
 100 105 110
 Val Glu Pro Thr Asn Cys Cys Pro Pro Ile Ser Thr Asn Ile Ile Asp

115					120					125					
Phe	Lys	Phe	Pro	Pro	Ser	Asn	Gln	Pro	Leu	Arg	Val	Arg	Ser	Ala	Ala
130						135					140				
His	Leu	Val	Asn	Lys	Asp	Tyr	Leu	Ala	Lys	Tyr	Glu	Lys	Ala	Val	Asn
145					150					155					160
Leu	Met	Lys	Asn	Leu	Pro	Ser	Asp	Asp	Pro	Arg	Ser	Phe	Ala	Gln	Gln
				165					170					175	
Ala	Lys	Val	His	Cys	Ala	Tyr	Cys	Asp	Gly	Gly	Tyr	His	Gln	Leu	Gly
			180					185					190		
Phe	Pro	Asp	Leu	Asp	Leu	Glu	Val	His	Phe	Ser	Trp	Leu	Phe	Phe	Pro
		195					200					205			
Tyr	His	Arg	Trp	Tyr	Leu	Tyr	Phe	His	Glu	Arg	Ile	Leu	Ala	Ser	Leu
	210					215					220				
Ile	Asn	Asp	Pro	Thr	Phe	Ala	Leu	Pro	Phe	Trp	Asn	Trp	Asp	Ala	Pro
225					230					235					240
Gly	Gly	Met	Gln	Leu	Pro	Ser	Met	Tyr	Ala	Asp	Pro	Lys	Ser	Pro	Leu
				245					250					255	
Tyr	Asp	Ser	Leu	Arg	Asn	Ala	Asn	His	Gln	Pro	Pro	Thr	Leu	Val	Asn
			260					265					270		
Leu	Asp	Phe	Thr	Ile	Glu	Asp	Pro	Asn	Ala	Glu	Ala	Asn	Ile	Ser	Thr
		275					280					285			
Asn	Leu	Thr	Thr	Met	Tyr	Arg	Gln	Leu	Val	Ser	Asn	Ala	Lys	Thr	Pro
	290					295					300				
Thr	Leu	Phe	Phe	Gly	Asn	Pro	Tyr	Arg	Ala	Gly	Asp	Gln	Pro	Asn	Pro
305					310					315					320
Gly	Gly	Gly	Ser	Val	Glu	Ser	Thr	Pro	His	Gly	Pro	Val	His	Ala	Trp
				325					330					335	
Thr	Gly	Asp	Ile	Asn	His	Pro	Thr	Met	Glu	Asp	Met	Gly	Asn	Leu	Tyr
			340					345					350		
Ala	Ala	Ala	Arg	Asp	Pro	Ile	Phe	Tyr	Cys	His	His	Ser	Asn	Val	Asp
		355					360					365			
Arg	Met	Trp	Ser	Ile	Trp	Lys	Thr	Leu	Gly	Gly	Lys	Arg	Arg	Asp	Leu
	370					375					380				
Thr	Asp	Pro	Asp	Trp	Leu	Glu	Ser	Ala	Phe	Leu	Phe	Tyr	Asp	Glu	Asn
385					390					395					400
Lys	Asn	Leu	Val	Arg	Val	Lys	Thr	Lys	Asp	Cys	Leu	Asp	Thr	Arg	Lys
				405					410					415	
Leu	Gly	Tyr	Val	Tyr	Gln	Asp	Val	Asp	Ile	Pro	Trp	Leu	Lys	Ser	Lys
			420					425					430		
Pro	Thr	Pro	Leu	Arg	Ser	Arg	Ala	Gln	Lys	Val	Glu	Leu	Thr	Pro	Leu

435					440					445						
Phe	Gly	Gly	Val	Ala	Ala	Ala	Ala	His	Ala	Ala	Glu	Thr	Ser	Arg	Asn	Val
450					455							460				
Lys	Phe	Pro	Leu	Val	Leu	Asp	Ser	Val	Val	Ser	Thr	Val	Val	Lys	Arg	
465					470					475					480	
Pro	Lys	Lys	Ser	Arg	Ser	Lys	Lys	Glu	Lys	Glu	Glu	Lys	Glu	Glu	Ile	
			485					490						495		
Leu	Val	Val	Glu	Gly	Ile	Glu	Phe	Glu	Ser	Ser	Thr	Gly	Val	Lys	Phe	
			500					505					510			
Asp	Val	Phe	Ile	Asn	Asp	Glu	Asp	Asp	Lys	Leu	Val	Lys	Pro	Asp	Asn	
		515					520					525				
Thr	Glu	Phe	Ala	Gly	Ser	Phe	Val	Ser	Val	Pro	His	Ser	His	Glu	His	
	530					535					540					
His	Lys	Asn	Asn	Lys	Lys	Ile	Val	Thr	Cys	Leu	Arg	Leu	Gly	Leu	Thr	
545				550						555					560	
Asp	Leu	Leu	Glu	Glu	Leu	Gly	Ala	Glu	Asp	Asp	Asp	Ser	Val	Leu	Val	
			565						570					575		
Thr	Leu	Val	Pro	Lys	Tyr	Gly	Lys	Gly	Arg	Val	Asn	Ile	Arg	Gly	Ile	
			580					585					590			
Lys	Ile	Asp	Phe	Val	Ser	Asp										
		595														

<210> 29
 <211> 685
 <212> DNA
 <213> Glycine max

 <220>
 <221> unsure
 <222> (478)
 <223> n = a, c, g or t

 <220>
 <221> unsure
 <222> (480)
 <223> n = a, c, g or t

 <220>
 <221> unsure
 <222> (555)
 <223> n = a, c, g or t

 <220>
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 <222> (570)
 <223> n = a, c, g or t

 <220>
 <221> unsure
 <222> (588)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (590)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (607)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (613)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (618)..(619)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (639)

<223> n = a, c, g or t

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<221> unsure

<222> (644)

<223> n = a, c, g or t

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<221> unsure

<222> (675)

<223> n = a, c, g or t

<400> 29

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catgcaaacc caccaaaccgt agcaaaccaa aacgccacca cgtttcgaaa gtgacatgca 180
acagtaacca aaacaccccca acaccaaacc cagaagaaga aagaccatca tacaacattc 240
taggaaaata tagaagggat gttctccttg gcattggggg cctttacggg gcatctgctc 300
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gcccaccaag atcttcttcc cctcctatag atttcaagtt gcctaaagga acaccctnan 480
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<210> 30

<211> 179

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (155)..(156)

<223> Xaa = any amino acid

<220>
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 <222> (172)
 <223> Xaa = any amino acid

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 20 25 30
 Ser Gln Ile Pro Cys Lys Pro Thr Lys Arg Ser Lys Pro Lys Arg His
 35 40 45
 His Val Ser Lys Val Thr Cys Asn Ser Asn Gln Asn Thr Pro Thr Pro
 50 55 60
 Asn Pro Glu Glu Glu Arg Pro Ser Tyr Asn Ile Leu Gly Lys Tyr Arg
 65 70 75 80
 Arg Asp Val Leu Leu Gly Ile Gly Gly Leu Tyr Gly Ala Ser Ala Leu
 85 90 95
 Ser Asn Thr Asn Pro Leu Ala Met Ala Ala Ala Pro Ile Leu Glu Pro
 100 105 110
 Asp Leu Glu His Cys Cys Ile Thr Asp Asp Val Pro Pro Lys Gly Val
 115 120 125
 Ile Glu Ala Gln Val Tyr Cys Cys Pro Pro Arg Ser Ser Ser Pro Pro
 130 135 140
 Ile Asp Phe Lys Leu Pro Lys Gly Thr Pro Xaa Xaa Leu Asp His Leu
 145 150 155 160
 Leu Asn Ser Ser Leu Met Glu Tyr Leu Glu Lys Xaa Lys Leu Ala Leu
 165 170 175
 Lys Arg Met

<210> 31
 <211> 1994
 <212> DNA
 <213> Glycine max

<400> 31
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 caaataccat gcaaaccctc caaacgtagc aaaccaaag gccatcatgt ttccaaagtg 180
 tcatgcaaca gtaacaaaa caccccaaca ccaaaccag aagaagaaaa accatcgta 240
 tacaacattc taggaaaaca taggagggat attctccttg gcattggggg cctttacggt 300
 gcttctgctc ttagcaaac caacccttta gccatggctg cagctcctat tctagagcct 360
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 ccccttaggg ttagaccacc tgctcaattt gtgaccgatg agtacctaga aaagtataag 540
 ttagccctta agcgcgatgag agagcttcca tctgatgatc ctcgaagttt caagcaacaa 600
 gctgatatcc attgtgctta ttgtgatggt ggctataagc aattagggtt cccagttgag 660

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accctactag ttaaaaggcc aaagcagttg aggagcaaga gggacaagga ggaagaggaa 1560
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gagtttgaga aggatgagtg aaaatatgtc actcatttac tactaaacat gcaaatgagt 1920
ttccaacatg caaatgagtt taaatttata tcagcatggt tagcaatttc aaagcaaaaa 1980
aaaaaaaaaa aaaa 1994

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<210> 32
<211> 619
<212> PRT
<213> Glycine max

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<400> 32
Met Ala Tyr Ile Ser Ser Leu Ser Ser Phe Ser Leu Ser Asn Phe Ser
 1             5             10             15

Ala Pro Leu Pro Ile Ser Ile Cys Ser Ser Ser Ser Ala Phe Leu Thr
      20             25             30

Ser Gln Ile Pro Cys Lys Pro Ser Lys Arg Ser Lys Pro Lys Gly His
      35             40             45

His Val Ser Lys Val Ser Cys Asn Ser Asn Gln Asn Thr Pro Thr Pro
      50             55             60

Asn Pro Glu Glu Glu Lys Pro Ser Ser Tyr Asn Ile Leu Gly Lys His
      65             70             75             80

Arg Arg Asp Ile Leu Leu Gly Ile Gly Gly Leu Tyr Gly Ala Ser Ala
      85             90             95

Leu Ser Asn Thr Asn Pro Leu Ala Met Ala Ala Ala Pro Ile Leu Glu
      100            105            110

Pro Asp Leu Glu His Cys Cys Ile Thr Asp Asp Val Pro Lys Gly Glu
      115            120            125

Ile Glu Lys Gln Val Tyr Cys Cys Pro Pro Lys Ser Ser Ser Pro Pro
      130            135            140

Ile Asp Phe Lys Leu Pro Lys Gly Thr Pro Leu Arg Val Arg Pro Pro
      145            150            155            160

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Ala	Gln	Phe	Val	Thr	Asp	Glu	Tyr	Leu	Glu	Lys	Tyr	Lys	Leu	Ala	Leu	
				165					170					175		
Lys	Arg	Met	Arg	Glu	Leu	Pro	Ser	Asp	Asp	Pro	Arg	Ser	Phe	Lys	Gln	
			180					185					190			
Gln	Ala	Asp	Ile	His	Cys	Ala	Tyr	Cys	Asp	Gly	Gly	Tyr	Lys	Gln	Leu	
		195					200					205				
Gly	Phe	Pro	Val	Glu	Leu	Asp	Phe	Lys	Val	His	Phe	Ser	Trp	Ile	Phe	
	210					215					220					
Phe	Pro	Phe	His	Arg	Trp	Tyr	Leu	Tyr	Phe	Tyr	Glu	Arg	Ile	Leu	Gly	
225					230					235					240	
Ser	Leu	Ile	Asp	Asp	Pro	Thr	Phe	Ala	Leu	Pro	Tyr	Trp	Asn	Trp	Asp	
				245					250					255		
Asn	Pro	Asp	Gly	Gly	Met	Val	Leu	Pro	Ser	Ile	Phe	Ala	Asp	Glu	Asp	
			260					265					270			
Ser	Pro	Leu	Tyr	Asp	Pro	Arg	Arg	Asn	Pro	Asp	Ile	Thr	Pro	Thr	Thr	
		275					280					285				
Leu	Val	Asp	Leu	Asn	Tyr	Gly	Ser	Gly	Lys	Glu	Pro	Ser	Val	Glu	Gln	
	290					295					300					
Asn	Leu	Gly	Val	Met	Tyr	Thr	Ser	Val	Val	Ser	Gly	Ala	Lys	Arg	Ala	
305					310					315					320	
Ser	Leu	Phe	His	Gly	Lys	Pro	Phe	Leu	Ala	Gly	Lys	Gln	Pro	Glu	Leu	
				325					330					335		
Ser	Gly	Gly	Thr	Val	Glu	Leu	Gly	Pro	His	Thr	Ala	Val	His	Arg	Trp	
			340					345					350			
Thr	Gly	Asp	Pro	Arg	Gln	Pro	Asn	Lys	Glu	Asp	Met	Gly	Arg	Phe	Tyr	
		355					360					365				
Ser	Ala	Gly	Arg	Asp	Pro	Ala	Phe	Tyr	Ser	His	His	Ala	Asn	Val	Asp	
	370					375					380					
Arg	Met	Trp	Asn	Ile	Trp	Lys	Thr	Ile	Pro	Ser	Gly	Lys	Arg	Arg	Asp	
385					390					395					400	
Phe	Lys	Asn	Arg	Asp	Trp	Leu	Glu	Thr	Ser	Phe	Phe	Phe	Tyr	Asp	Glu	
				405					410					415		
Asn	Lys	Thr	Leu	Val	Arg	Val	Lys	Val	Lys	Asp	Ser	Leu	Asp	Thr	Asn	
			420					425					430			
Lys	Met	Gly	Tyr	Val	Tyr	Gln	Asp	Val	Ala	Ile	Pro	Trp	Leu	Glu	Lys	
		435					440					445				
Lys	Pro	Lys	Pro	Lys	Arg	Thr	Arg	Lys	Ala	Lys	Lys	Val	Ala	Phe	Ala	
		450				455					460					
Gln	Gln	Phe	Gly	Gly	Ile	Gly	Ala	Ala	Met	Ala	Ala	Glu	Thr	Gly	Pro	
465					470					475					480	

Ser Ser Lys Phe Pro Leu Thr Leu Leu Asp Ser Lys Val Thr Leu Leu
 485 490 495
 Val Lys Arg Pro Lys Gln Leu Arg Ser Lys Arg Asp Lys Glu Glu Glu
 500 505 510
 Glu Glu Val Leu Val Ile Asp Gly Ile Glu Phe Asp Gly Asp Asp Asp
 515 520 525
 Val Lys Phe Asp Val Tyr Ile Thr Asp Glu Asp Val Glu Asp Ile Gly
 530 535 540
 Pro Glu Ser Thr Glu Phe Ala Gly Ser Phe Ser Thr Leu Gly His Ser
 545 550 555 560
 His Ser Asn Met Asn Met Asp Lys Lys Ile Lys Thr Ser Leu Thr Leu
 565 570 575
 Gly Ile Thr Asp Leu Leu Glu Asp Leu Asp Ala Glu Asn Asp Asp Ser
 580 585 590
 Val Leu Val Thr Leu Val Pro Arg Ser Glu Asn Val Thr Ile Thr Ile
 595 600 605
 Gln Asn Ile Lys Ile Glu Phe Glu Lys Asp Glu
 610 615

<210> 33
 <211> 2028
 <212> DNA
 <213> Glycine max

<400> 33
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 tgcaatggta accctagaaa taggagggac attctgatcg gccttggagg actctatggg 180
 gctacaacaa gtctcacaag taacaacact ggttctgcat ttggtgcttc attgtcgcct 240
 ccagatccaa ctaactgcgt tcaaccggac ccagaaaaag accctttttg cccaccaccc 300
 cccttcaaag actacgagct ccctccacac gatgacaaga cattaccctt tcgaattaga 360
 ccagctgctc atttgggtcac tgatgattac atagccaagt acgaggaagc cgtgaggcgc 420
 atgcaagacc ttccacctga tgatcctcgc agtttcatgc aacaggccaa tgtccaccgt 480
 gcctactgcg atgggtcgcg ctatactcaa aagggtctcg ctgactacaa gcttgacgtt 540
 cacggctcct ggatattctt tccttggcac cgctgggtatc tctatttcta tgagaaaatc 600
 ttggggaaga tgatcggtga cccactttc gctcttccgt tttggaactg ggacaatccc 660
 gccggcatga gaatccctcc cattttcaca gacaaaagtt cgcctctcta cgacgaacac 720
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 aatcaccacg acatgggggtt gttggctacg gctgcaaaag atcccatttt ctttgctcac 1080
 cattcaaacg tcgataggat gtggaacata tgggaagacag aattgctgga tgggaagaag 1140
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aacatcacca aagcttcttt caaattgcc a ttaacgtata agttgaaaga cttggggagta 1680
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attatgtgtg tgctactgct agggtttggt cctccaaggg atactctatc tgcattttgt 1860
tgtttcttaa ttagtggtgt gtagttatct tccttggaac ttaatagatc cctttcatct 1920
gtgagggata ctatgttatt gttataataa atgtttgttt tattgttaca tttgtttata 1980
atacaatata actcctaata tcctttttaa aaaaaaaaaa aaaaaaaa 2028

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<210> 34
<211> 597
<212> PRT
<213> Glycine max

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<400> 34
Ala Arg Gly Ser Leu Leu Asn Leu Ser Ala Ser Ile Pro Ile Ser Ser
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Ser Val Cys Met Phe Pro Pro Ser Lys Lys Pro Ser Lys Ala Thr Lys
          20          25          30

Arg Arg His Ala Trp Glu Val Ala Cys Asn Gly Asn Pro Arg Asn Arg
          35          40          45

Arg Asp Ile Leu Ile Gly Leu Gly Gly Leu Tyr Gly Ala Thr Thr Ser
          50          55          60

Leu Thr Ser Asn Asn Thr Gly Ser Ala Phe Gly Ala Ser Leu Ser Pro
          65          70          75

Pro Asp Pro Thr Asn Cys Val Gln Pro Asp Pro Glu Lys Asp Pro Phe
          85          90          95

Cys Pro Pro Pro Pro Phe Lys Asp Tyr Glu Leu Pro Pro His Asp Asp
          100          105          110

Lys Thr Leu Pro Leu Arg Ile Arg Pro Ala Ala His Leu Val Thr Asp
          115          120          125

Asp Tyr Ile Ala Lys Tyr Glu Glu Ala Val Arg Arg Met Gln Asp Leu
          130          135          140

Pro Pro Asp Asp Pro Arg Ser Phe Met Gln Gln Ala Asn Val His Arg
          145          150          155          160

Ala Tyr Cys Asp Gly Arg Gly Tyr Thr Gln Lys Gly Phe Ala Asp Tyr
          165          170          175

Lys Leu Asp Val His Gly Ser Trp Ile Phe Phe Pro Trp His Arg Trp
          180          185          190

Tyr Leu Tyr Phe Tyr Glu Lys Ile Leu Gly Lys Met Ile Gly Asp Pro
          195          200          205

Thr Phe Ala Leu Pro Phe Trp Asn Trp Asp Asn Pro Ala Gly Met Arg
          210          215          220

Ile Pro Pro Ile Phe Thr Asp Lys Ser Ser Pro Leu Tyr Asp Glu His
          225          230          235          240

Arg Asn Ser Asp His Val Asn Ala Phe Ile Asp Leu Asp Tyr Lys Lys

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245										250					255				
Asp	Asp	Ser	Pro	Val	Lys	Pro	Pro	Gln	Thr	Ile	Leu	Trp	Pro	Pro	Val				
			260					265					270						
Glu	Lys	Lys	Asn	Asn	Ser	Ile	Val	Asp	Asn	Leu	Ile	Val	Asn	Asn	Leu				
		275					280					285							
Ile	Lys	Val	Tyr	Thr	Ala	Val	Ala	Ser	Lys	Thr	Asn	Ser	Ser	Pro	Asp				
	290					295					300								
Tyr	Phe	Leu	Gly	Pro	Ala	Phe	Glu	Ala	Gly	Ser	Ala	Pro	Gln	Gln	His				
305					310					315					320				
Phe	Gly	Ser	Leu	Glu	Ser	Leu	His	Asn	Thr	Val	His	Ser	Trp	Thr	Gly				
				325					330					335					
Glu	Arg	Glu	Asn	Asn	His	His	Asp	Met	Gly	Leu	Leu	Ala	Thr	Ala	Ala				
			340					345					350						
Lys	Asp	Pro	Ile	Phe	Phe	Ala	His	His	Ser	Asn	Val	Asp	Arg	Met	Trp				
		355					360					365							
Asn	Ile	Trp	Lys	Thr	Glu	Leu	Leu	Asp	Gly	Arg	Arg	Phe	Asp	His	Lys				
	370					375					380								
Ser	Asp	Asp	Trp	Leu	Glu	Ser	Ser	Phe	Phe	Phe	Tyr	Asp	Glu	Asn	Lys				
385					390					395					400				
Asn	Tyr	Val	Arg	Val	Lys	Val	Lys	Asp	Cys	Leu	Asp	Ser	Lys	Lys	Met				
			405					410						415					
Gly	Tyr	Asp	Tyr	Gln	Arg	Val	Asp	Leu	Pro	Trp	Leu	Leu	Ala	Gly	Glu				
		420					425						430						
Leu	Ile	Lys	Pro	Lys	Lys	Glu	Ile	Ile	Leu	Leu	Arg	Ser	Lys	Pro	Glu				
	435					440						445							
Ala	Ser	Thr	Phe	Lys	Thr	Leu	Gln	Leu	Pro	Leu	Pro	Leu	Glu	Ser	Ile				
	450					455					460								
Glu	Arg	Thr	Asn	Val	Lys	Arg	Pro	Lys	Pro	Arg	Ser	Arg	Asn	Glu	Asn				
465				470					475					480					
Glu	Glu	Glu	Glu	Glu	Gly	Val	Glu	Glu	Val	Leu	Val	Ile	Asp	Val	Glu				
			485				490						495						
Tyr	Asp	Ser	Thr	Asp	Gly	Val	Arg	Phe	Asp	Val	Phe	Ile	Asn	Asp	Gln				
	500						505						510						
Gly	Asp	Asn	Glu	Ile	Gly	Pro	Gln	Asp	Ser	Glu	Phe	Ala	Gly	Ser	Phe				
	515						520					525							
Val	Thr	Leu	Pro	His	Ser	Pro	His	Val	Asn	His	Asn	Asn	Ile	Thr	Lys				
	530					535					540								
Ala	Ser	Phe	Lys	Leu	Pro	Leu	Thr	Tyr	Lys	Leu	Lys	Asp	Leu	Gly	Val				
545				550					555					560					
Thr	Lys	Asp	Asp	Asp	Ser	Ile	Ser	Val	Thr	Leu	Ala	Pro	Ile	Tyr	Gly				

565

570

575

Asp Lys Pro Val Thr Ile Lys Asp Val Arg Ile Lys Arg Val Tyr Pro
580 585 590

Glu Val Asp Asp Glu
595

<210> 35
<211> 2260
<212> DNA
<213> Glycine max

<400> 35
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gtcttgctga tgcccttagt ttccttactc aacaatgatt tctctatctt caccattaaa 180
accatttcat acctagtttc ctttagtgaa aagccaaacc attactctaa tttcagcatt 240
attccataca aagcccaaaa tagtaaacaa aatggccaca tcaccacaaa ctccaatgga 300
agagacaaac cacgtctttg gaggaagcc ttcattggct tcaaaaatac tcacgagcca 360
tcttcgaata tttctcgagc aatatccctt aatgtaagca agtggtttcc cgttgagtta 420
ccttcttttg caataaccaa ttcccattgt tgtccacctt gaccacctcc ttctaagatc 480
atagatttca aagattttgc ttctccaaac gccacgcttc gagtaagaaa accgggtcac 540
atggttagatg aggagtacat agcaaaactt gaaaaggcca ttgcactcat gaaagcactc 600
cctgatgatg acccacgtaa tttcatacaa caagcaaagg tccattgtgc ttattgtaac 660
ggtgcctatc acctacccca tccctttcag aacacaaaac tcaacattca caggtccttg 720
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ctcggtgacc cgaactttgc cttaccgttt tgggaattggg atgctgtaga agggatgcaa 840
atgccaccat atttcgcaaa ccctaactcg tcgctctatc acaaactccg aaaccccaag 900
cacttgccac cgcaagtggg tgacctgaac tatgatccat ttgactttaa tgatgataca 960
ccttctcatc aacaagtttc gtataatcta gccttcatgt acaagcaaat ggtgctagca 1020
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attggctcta tagaggctgc tcctcataac acggttcata aatgggttggt tgctgctgat 1140
aagccacacc aggaggacat gggaacgttc tacacagctg ctagagatcc cgttttctat 1200
ccgcatacaca cgaactcgga tcgactgtgg gggatattgga aaaaattggg agaaggaaga 1260
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aataaaaaat tgagtttgat gtaaaaaaaa aaaaaaaaaa 2260

<210> 36
<211> 601
<212> PRT
<213> Glycine max

<400> 36
Met Ser Thr Pro Ser Lys Leu Leu Ser Leu Phe Phe Val Leu Ile Val

1	5	10	15
Leu Leu Met Pro Leu Val Ser Leu Leu Asn Asn Asp Phe Ser Ile Phe	20	25	30
Thr Ile Lys Thr Ile Ser Tyr Leu Val Ser Phe Ser Glu Lys Pro Asn	35	40	45
His Tyr Ser Asn Phe Ser Ile Ile Pro Tyr Lys Ala Gln Asn Ser Lys	50	55	60
Gln Asn Gly His Ile Thr Thr Asn Ser Asn Gly Arg Asp Lys Pro Arg	65	70	75
Leu Trp Arg Lys Ala Phe Ile Gly Phe Lys Asn Thr His Glu Pro Ser	85	90	95
Ser Asn Ile Ser Arg Ala Ile Ser Leu Asn Val Ser Lys Cys Phe Pro	100	105	110
Val Glu Leu Pro Ser Phe Ala Ile Thr Asn Ser His Cys Cys Pro Pro	115	120	125
Arg Pro Pro Pro Ser Lys Ile Ile Asp Phe Lys Asp Phe Ala Ser Pro	130	135	140
Asn Ala Thr Leu Arg Val Arg Lys Pro Ala His Met Val Asp Glu Glu	145	150	155
Tyr Ile Ala Lys Leu Glu Lys Gly Ile Ala Leu Met Lys Ala Leu Pro	165	170	175
Asp Asp Asp Pro Arg Asn Phe Ile Gln Gln Ala Lys Val His Cys Ala	180	185	190
Tyr Cys Asn Gly Ala Tyr His Leu Pro His Pro Phe Gln Asn Thr Lys	195	200	205
Leu Asn Ile His Arg Ser Trp Phe Phe Phe Pro Phe His Arg Trp Tyr	210	215	220
Ile Tyr Phe Phe Glu Arg Ile Leu Gly Ser Leu Leu Gly Asp Pro Asn	225	230	235
Phe Ala Leu Pro Phe Trp Asn Trp Asp Ala Val Glu Gly Met Gln Met	245	250	255
Pro Pro Tyr Phe Ala Asn Pro Asn Ser Ser Leu Tyr His Lys Leu Arg	260	265	270
Asn Pro Lys His Leu Pro Pro Gln Val Val Asp Leu Asn Tyr Asp Pro	275	280	285
Phe Asp Phe Asn Asp Asp Thr Pro Ser His Gln Gln Val Ser Tyr Asn	290	295	300
Leu Ala Phe Met Tyr Lys Gln Met Val Leu Ala Ser Thr Lys Glu Leu	305	310	315
Phe Met Gly Ser Pro Phe Arg Leu Gly Asp Asn Pro Thr Pro Gly Ile			

<222> (16)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (60)
 <223> n = a, c, g or t

<400> 37
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 ccgcgcgcgc caagtacgac gacgccgttc aaaccaacct gtgcaccata tacctgcagc 180
 aagtccgtga cggcaagggc ccccggtgctt tcctcggcga gaagctgtgc agcgaccagg 240
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 c 1141

<210> 38
 <211> 358
 <212> PRT
 <213> Zea mays

<220>
 <221> UNSURE
 <222> (5)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (20)
 <223> Xaa = any amino acid

<220>
 <221> UNSURE
 <222> (179)
 <223> Xaa = any amino acid

<400> 38
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 Leu Leu Asp Xaa Asp Tyr Leu Lys Lys Pro Arg Arg Asp Thr Ile Pro
 20 25 30
 Phe Glu Pro Pro Thr Asp Pro Ala Ala Arg Ala Lys Tyr Asp Asp Ala
 35 40 45

Val	Gln	Thr	Asn	Leu	Cys	Thr	Ile	Tyr	Leu	Gln	Gln	Val	Arg	Asp	Gly	
50						55					60					
Lys	Gly	Pro	Arg	Ala	Phe	Leu	Gly	Glu	Lys	Leu	Cys	Ser	Asp	Gln	Gly	
65					70					75					80	
Thr	Leu	Glu	Arg	Met	Ala	His	Thr	Thr	Val	His	Val	Trp	Thr	Gly	Arg	
				85					90					95		
Ala	Asn	Pro	Ala	Thr	Cys	Ser	Ala	Glu	Gln	Gly	Gly	Val	Val	Gly	His	
			100					105					110			
Asp	Gly	Lys	Pro	His	Cys	Gln	Val	Asp	Met	Gly	Phe	Leu	Gly	Thr	Ala	
		115					120					125				
Gly	Arg	Asp	Pro	Leu	Phe	Tyr	Ser	His	His	Ala	Asn	Val	Asp	Arg	Met	
	130					135					140					
Trp	His	Ile	Trp	Ser	Thr	Arg	Leu	Gly	Gly	Lys	Gly	Phe	Asp	Asp	Pro	
145					150					155					160	
Glu	Trp	Leu	Asp	Thr	Ser	Phe	Val	Phe	Tyr	Asp	Asp	Tyr	Arg	Ser	Arg	
				165					170					175		
Gly	Trp	Xaa	Gln	Met	Lys	Phe	Arg	Asp	Val	Leu	Asn	Ala	Thr	Arg	Leu	
			180					185					190			
Gly	Tyr	Thr	Tyr	Asp	Lys	Glu	Ser	Glu	Ala	Ala	Leu	Pro	Trp	Leu	Asn	
		195					200					205				
Ser	Lys	Pro	Thr	Arg	Phe	Ser	Gly	Gly	Gly	Lys	Ala	Lys	Ala	Lys	Ala	
	210					215					220					
Ala	Pro	Lys	Val	Ala	Ser	Glu	Phe	Pro	Leu	Thr	Leu	Thr	Asp	Glu	Ala	
225					230					235					240	
Val	Asp	Val	Pro	Ala	Val	Ala	Val	Pro	Ala	Arg	Gln	Ala	Gly	Lys	Asp	
				245					250					255		
Leu	Val	Leu	Leu	Ile	Glu	Gly	Ile	Glu	Tyr	Asp	Pro	Gln	Ile	Asn	Asn	
			260					265					270			
Lys	Phe	Asp	Val	Val	Ile	Asn	Val	Ala	Arg	Glu	Asp	Ala	Ala	Arg	Val	
		275					280					285				
Gly	Pro	Lys	Asp	Ser	Glu	Tyr	Ala	Gly	Ser	Phe	Ser	Ala	Val	Pro	Ser	
	290					295					300					
Ser	Asn	Ala	Ala	Gly	Gly	Thr	Leu	Val	Gly	Lys	Phe	Thr	Leu	Ala	Leu	
305					310					315					320	
Asp	Gly	Val	Leu	Ala	Asp	Leu	Gly	Leu	Ala	Gly	Ala	Ser	Ala	Val	Asp	
				325					330					335		
Ile	Val	Leu	Val	Pro	His	Thr	Glu	Gly	Glu	Ile	Lys	Leu	Tyr	Leu	Pro	
			340					345					350			
Pro	Thr	Ile	Glu	Asn	Ala											
		355														

<210> 39
 <211> 2173
 <212> DNA
 <213> Zea mays

<400> 39
 gcgtggcaac gtccaaaatc cagaccgctg gtaggagtat ctcgtagaca ttgaacaacg 60
 gctgcatggc gagcgccctgc gccacctcca tccccctcgt ctggcgccc tctgcatgcc 120
 cgtccaagaa gaccaccgtc gccaggttcc ggcgccgcac ggcgacgtgc agggccagca 180
 gcggcggttg cgggtggccgg ggcggcgaaa atgatggcct cctttggctg ccccgcggg 240
 acgtgatgct caacggcctg tccagtgtcg ccgcccgggt cgccgtgtac ccgggcgtcg 300
 cgtccggcgc ggatgcgggtg tgcaccaggg ccgacaaggt gaacgagaag accgtgcagt 360
 gcacggaccc ggccgggcag cttccgtgcc ctctggtgtc gccgacggac cccgtggact 420
 tcaagccgga aagcaagggt acgcgcatcc ggagccgggt gcatctcctg agccgggagt 480
 accaggagaa gtacaaggag gccgtcgcga agatgaaggc gctaccggaa gagaacccgc 540
 tgagcttcgc ggcccaggcg gccatccacc aggttactg cgacgcctac tacaagtacg 600
 acccgacggc caaggacgcg ccgttcgacg tgcacttctc gtggatcttc gcgcgtggc 660
 accgcatgta catctacttc tacgagcgcg ccctcgggca gctcatcgcc gacgacacct 720
 tcgcgtgcc gttctggaac tgggacacgc cggccggcat ggtggtgccg ccactcttca 780
 aggactccat gggcaacccg ctgtacgacc ccaacaggaa cccgtcgaac gtcgacgcgc 840
 tgggtggactt agactacctc aacgacagga atgctggagc catcccttcc aagggccac 900
 gggacgaaaa gtacaaggaa cttgtgaaca agaactgtg caccgtatac acccagcaaa 960
 tacgtagcgg caagggcgcc gagtcgttcc tgggcgagaa gtactgcacc gacatcgggt 1020
 caagcacgag cagcatgggt tcgctggagc ggatggcgca cactgccgtg cacgtctggg 1080
 tcggcaaggc gggcccgacg ccttcctcgg aggcgtgcag tgccgtacc ggcggttcc 1140
 cgaaccacac caaaggcggg tacagctgca acaacgacat ggggttctctg gggtcggcgg 1200
 gacacgaccc gctcttctac tcgcaccact ccaacgtcga ccgcatgtgg cacatctggt 1260
 cgaccaggct cggcgggcggg cagggcacat cggaggcgga ctggctcgac accagcttcg 1320
 tcttctacga cgacgtcaag agcccgcgga aggtgcgcac cagggtccgc gacgtcctgg 1380
 acacgcgcga cctcggtac acgtacgacg ccgagtcgca caaggacctg ccatggctgc 1440
 gctgcaagat ctcgctcgctg gtgccccacg gcaaggacag cccgcgaggt tcgtcgctcg 1500
 caaggaaggc ggcgccgggtg ttcccgtcgt ccctgactaa gggccagggtg gtggaagtgc 1560
 cggccgtgcc tgtgccggcc aaggacccgg ggaaggagca gctgctgggtg atcgagggca 1620
 tcgagtacga cccccaggcg aacaataagt tcgacgtcgc catcaacctg cccgcggaca 1680
 aagcgttgca ggtaggccca cagtacaagg agtacgccg aagcttcgcc gtcgtgccgg 1740
 gctccggcgc cgggaagacg cggaaaagtga agctctccct gtgcatcacc gaagtgcgtg 1800
 tcgatatcga cgtgacggc gataaaaccg tcgacgtcgt tatcgtgccg cgcacaaatg 1860
 ctaagatcac gctcaacgct cgccccacca tcaagaatcg gaactaggag ctagtgtgta 1920
 ctagtgtcga tcaagcacac tgtacgtacg tacgtatgta ctgcatcgcg tggtcattca 1980
 tcgaccatca tcgtttatat gctgtcacgc acagcgcggg ccggccggta ggggtgtcggc 2040
 aataataaac gcggccagtg ttgcattatt gtgtgtttta tttcacaagg attaggagcg 2100
 agccaatggg agattctaag gaataaataa cattgttatg aatgatatgg ttatgtttta 2160
 gagactaatt gcg 2173

<210> 40
 <211> 613
 <212> PRT
 <213> Zea mays

<400> 40
 Met Ala Ser Ala Cys Ala Thr Ser Ile Pro Leu Val Ser Ala Pro Ser
 1 5 10 15
 Ala Cys Pro Ser Lys Lys Thr Thr Val Ala Arg Phe Arg Arg Arg Thr
 20 25 30
 Ala Thr Cys Arg Ala Ser Ser Gly Gly Gly Gly Gly Arg Gly Gly Glu
 35 40 45

Asn	Asp	Gly	Leu	Leu	Trp	Leu	Pro	Arg	Arg	Asp	Val	Met	Leu	Asn	Gly	50	55	60
Leu	Ser	Ser	Val	Ala	Ala	Gly	Leu	Ala	Trp	Tyr	Pro	Gly	Val	Ala	Ser	65	70	75
Gly	Ala	Asp	Ala	Val	Cys	Thr	Arg	Ala	Asp	Lys	Val	Asn	Glu	Lys	Thr	85	90	95
Val	Gln	Cys	Thr	Asp	Pro	Ala	Gly	Gln	Leu	Pro	Cys	Pro	Leu	Val	Ser	100	105	110
Pro	Thr	Asp	Pro	Val	Asp	Phe	Lys	Pro	Glu	Ser	Lys	Val	Thr	Arg	Ile	115	120	125
Arg	Gln	Pro	Val	His	Leu	Leu	Ser	Arg	Glu	Tyr	Gln	Glu	Lys	Tyr	Lys	130	135	140
Glu	Ala	Val	Ala	Lys	Met	Lys	Ala	Leu	Pro	Glu	Glu	Asn	Pro	Leu	Ser	145	150	155
Phe	Ala	Ala	Gln	Ala	Ala	Ile	His	Gln	Ala	Tyr	Cys	Asp	Ala	Tyr	Tyr	165	170	175
Lys	Tyr	Asp	Pro	Thr	Ala	Lys	Asp	Ala	Pro	Phe	Asp	Val	His	Phe	Ser	180	185	190
Trp	Ile	Phe	Ala	Pro	Trp	His	Arg	Met	Tyr	Ile	Tyr	Phe	Tyr	Glu	Arg	195	200	205
Ala	Leu	Gly	Gln	Leu	Ile	Gly	Asp	Asp	Thr	Phe	Ala	Leu	Pro	Phe	Trp	210	215	220
Asn	Trp	Asp	Thr	Pro	Ala	Gly	Met	Val	Val	Pro	Pro	Leu	Phe	Lys	Asp	225	230	235
Ser	Met	Gly	Asn	Pro	Leu	Tyr	Asp	Pro	Asn	Arg	Asn	Pro	Ser	Asn	Val	245	250	255
Asp	Ala	Leu	Val	Asp	Leu	Asp	Tyr	Leu	Asn	Asp	Arg	Asn	Ala	Glu	Pro	260	265	270
Ile	Pro	Phe	Lys	Gly	Pro	Arg	Asp	Glu	Lys	Tyr	Lys	Glu	Leu	Val	Asn	275	280	285
Lys	Asn	Leu	Cys	Thr	Val	Tyr	Thr	Gln	Gln	Ile	Arg	Ser	Gly	Lys	Gly	290	295	300
Ala	Glu	Ser	Phe	Leu	Gly	Glu	Lys	Tyr	Cys	Thr	Asp	Ile	Gly	Ser	Ser	305	310	315
Thr	Ser	Ser	Met	Gly	Ser	Leu	Glu	Arg	Met	Ala	His	Thr	Ala	Val	His	325	330	335
Val	Trp	Val	Gly	Lys	Ala	Gly	Pro	Thr	Pro	Ser	Ser	Glu	Ala	Cys	Ser	340	345	350
Ala	Ala	Thr	Gly	Gly	Phe	Pro	Asn	His	Thr	Lys	Gly	Gly	Tyr	Ser	Cys	355	360	365

Asn Asn Asp Met Gly Phe Leu Gly Ser Ala Gly His Asp Pro Leu Phe
 370 375 380
 Tyr Ser His His Ser Asn Val Asp Arg Met Trp His Ile Trp Ser Thr
 385 390 395 400
 Arg Leu Gly Gly Gly Gln Gly Ile Thr Glu Ala Asp Trp Leu Asp Thr
 405 410 415
 Ser Phe Val Phe Tyr Asp Asp Val Lys Ser Pro Arg Lys Val Arg Ile
 420 425 430
 Arg Phe Arg Asp Val Leu Asp Thr Arg Asp Leu Gly Tyr Thr Tyr Asp
 435 440 445
 Ala Glu Ser Asp Lys Asp Leu Pro Trp Leu Arg Cys Lys Ile Ser Ser
 450 455 460
 Leu Val Pro His Gly Lys Asp Ser Pro Pro Arg Ser Ser Ser Ala Arg
 465 470 475 480
 Lys Ala Ala Pro Val Phe Pro Leu Ala Leu Thr Lys Gly Gln Val Val
 485 490 495
 Glu Val Pro Ala Val Pro Val Pro Ala Lys Asp Pro Gly Lys Glu Gln
 500 505 510
 Leu Leu Val Ile Glu Gly Ile Glu Tyr Asp Pro Gln Ala Asn Asn Lys
 515 520 525
 Phe Asp Val Ala Ile Asn Leu Pro Ala Asp Lys Ala Leu Gln Val Gly
 530 535 540
 Pro Gln Tyr Lys Glu Tyr Ala Gly Ser Phe Ala Val Val Pro Gly Ser
 545 550 555 560
 Gly Ala Gly Lys Thr Arg Lys Val Lys Leu Ser Leu Cys Ile Thr Glu
 565 570 575
 Val Leu Phe Asp Ile Asp Ala Asp Gly Asp Lys Thr Val Asp Val Val
 580 585 590
 Ile Val Pro Arg Thr Asn Ala Lys Ile Thr Leu Asn Ala Arg Pro Thr
 595 600 605
 Ile Lys Asn Arg Asn
 610
 <210> 41
 <211> 409
 <212> DNA
 <213> Zea mays
 <220>
 <221> unsure
 <222> (409)
 <223> n = a, c, g or t
 <400> 41
 ccagctgatt tgtccacgcg gcatggcgac ggccagcgcc gcttcaagct tctcgtccc 60

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ggcgactgct atcgccccga caccctctgc atgcccattc acggttccca agaacaagaa 120
gaatgctgcc ggccggcgcc ggcgcacatt gcagtgcagg gccagcgcc ggcggggcga 180
cgacgaagac agccgcctcc tctggctgcc ccggcgggaa gtgctgaccg gtctgggcgg 240
cgtggccgcc agcttcgtcg ggtacccgga tctggcttcc atcgccctgg aagcgaaccc 300
cgtggagagc tgccggcgcc gcgagaaggt gacggagaag ctggtggagt gctcggaccc 360
gaacagagac ttcccgtgcc cgccggcgtc acgggtcccc atcgtggan 409

```

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<210> 42
<211> 123
<212> PRT
<213> Zea mays

```

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<400> 42
Met Ala Thr Ala Ser Ala Ala Ser Ser Phe Leu Val Pro Ala Thr Ala
  1             5             10             15

Ile Ala Pro Thr Pro Ser Ala Cys Pro Ser Thr Val Pro Lys Asn Lys
          20             25             30

Lys Asn Ala Ala Gly Arg Arg Arg Arg Thr Leu Gln Cys Arg Ala Ser
          35             40             45

Gly Arg Arg Gly Asp Asp Glu Asp Ser Arg Leu Leu Trp Leu Pro Arg
          50             55             60

Arg Glu Val Leu Thr Gly Leu Gly Gly Val Ala Ala Ser Phe Val Gly
          65             70             75             80

Tyr Pro Asp Leu Ala Ser Ile Ala Leu Glu Ala Asn Pro Val Glu Ser
          85             90             95

Cys Arg Arg Gly Glu Lys Val Thr Glu Lys Leu Val Glu Cys Ser Asp
          100            105            110

Pro Asn Arg Asp Phe Pro Cys Pro Pro Ala Ser
          115            120

```

```

<210> 43
<211> 497
<212> DNA
<213> Glycine max

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<220>
<221> unsure
<222> (325)
<223> n = a, c, g or t

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<220>
<221> unsure
<222> (397)
<223> n = a, c, g or t

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<220>
<221> unsure
<222> (411)
<223> n = a, c, g or t

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<220>
<221> unsure
<222> (422)

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<223> n = a, c, g or t

<220>

<221> unsure

<222> (438)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (441)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (453)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (463)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (467)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (477)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (487)

<223> n = a, c, g or t

<220>

<221> unsure

<222> (489)

<223> n = a, c, g or t

<400> 43

gacctagact	acaacggcgt	tgaagaccaa	tcctcaacac	aagaacaaat	atcaaccaat	60
ctcaacacca	tgtaccggca	actgggtgtca	agttcaaaga	ctccaacgct	cttcttcggt	120
agcccttacc	gtgcaggaga	agatagtgat	cccgggtggtg	gcactgtgga	gaacattcct	180
cacgggtccgg	tccatatatg	gaccgggtgat	aacacacaac	ctaactttga	ggacatgggg	240
actctctatt	ctgctgctag	agaccctatt	ttctattctc	accacgctaa	tgtggataga	300
atgtgggtcca	tatggaaaac	tcttngagga	aagagagtga	catcaaagac	cctgattggt	360
ggaatctggg	ttctttctac	gatgagaaca	agaatcntgt	cgtgtgaggt	naggattgtc	420
tngtactaga	agcttgantg	ntaccaaagt	atntgtccgt	ggnaaancta	gccaaaancgg	480
tttcgangng	gtcaaga					497

<210> 44

<211> 112

<212> PRT

<213> Glycine max

<220>

<221> UNSURE

<222> (109)
 <223> Xaa = any amino acid

<400> 44
 Asp Leu Asp Tyr Asn Gly Val Glu Asp Gln Ser Ser Thr Gln Glu Gln
 1 5 10 15
 Ile Ser Thr Asn Leu Asn Thr Met Tyr Arg Gln Leu Val Ser Ser Ser
 20 25 30
 Lys Thr Pro Thr Leu Phe Phe Gly Ser Pro Tyr Arg Ala Gly Glu Asp
 35 40 45
 Ser Asp Pro Gly Gly Gly Thr Val Glu Asn Ile Pro His Gly Pro Val
 50 55 60
 His Ile Trp Thr Gly Asp Asn Thr Gln Pro Asn Phe Glu Asp Met Gly
 65 70 75 80
 Thr Leu Tyr Ser Ala Ala Arg Asp Pro Ile Phe Tyr Ser His His Ala
 85 90 95
 Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Xaa Gly Lys Arg
 100 105 110

<210> 45
 <211> 713
 <212> DNA
 <213> Glycine max

<220>
 <221> unsure
 <222> (579)
 <223> n = a, c, g or t

<220>
 <221> unsure
 <222> (618)
 <223> n = a, c, g or t

<400> 45
 ggtccctcct gaacctgtct gcatccattc ccattttcttc ttccgtatgc atgttcccac 60
 cgtctaaaaa acctagcaaa gcaacaaaac ggcgtcatgc ttgggaagta gcatgcaatg 120
 gtaaccctag aaataggagg gacattctga tcggccttgg aggactctat ggtgctacaa 180
 caagtctcac aagtaacaac actggttctg catttggtgc ttcattgtcg cctccagatc 240
 caactaactg cgttcaaccg gaccagaaaa aagacccttt ttgcccacca ccccttcaa 300
 agactacgag ctccctccac acgatgacaa gacattaccc cttcgaatta gaccaagctg 360
 ctcatcttgg cactgatgat tacatagcca agtacgagga agccgtgagg cgcattgcaag 420
 accttccacc tgatgatcct cgcagtttca tgcaacaagc caatgtccac cgtgcctact 480
 gcgatgggtc cggctatatc aaaagggttc gctgactaca agcttgacgt tcacggtcct 540
 ggatatacct ccctgggacg ctggtactcc atttctaana aaaacctggg aagatgatcg 600
 atgaccactc tcgctctncc ttttggaaac ggacaatccc gccggatgag atcctcccat 660
 ttcacaagac aaattcactc tctacgacga acacaagaat acgttaatgt taa 713

<210> 46
 <211> 162
 <212> PRT
 <213> Glycine max

<400> 46

Ser	Leu	Leu	Asn	Leu	Ser	Ala	Ser	Ile	Pro	Ile	Ser	Ser	Ser	Val	Cys			
1				5					10					15				
Met	Phe	Pro	Pro	Ser	Lys	Lys	Pro	Ser	Lys	Ala	Thr	Lys	Arg	Arg	His			
			20					25					30					
Ala	Trp	Glu	Val	Ala	Cys	Asn	Gly	Asn	Pro	Arg	Asn	Arg	Arg	Asp	Ile			
		35					40					45						
Leu	Ile	Gly	Leu	Gly	Gly	Leu	Tyr	Gly	Ala	Thr	Thr	Ser	Leu	Thr	Ser			
	50					55					60							
Asn	Asn	Thr	Gly	Ser	Ala	Phe	Gly	Ala	Ser	Leu	Ser	Pro	Pro	Asp	Pro			
65					70				75					80				
Thr	Asn	Cys	Val	Gln	Pro	Asp	Pro	Glu	Lys	Asp	Pro	Phe	Cys	Pro	Pro			
				85					90					95				
Pro	Pro	Ser	Lys	Thr	Thr	Ser	Ser	Leu	His	Thr	Met	Thr	Arg	His	Tyr			
			100					105					110					
Pro	Phe	Glu	Leu	Asp	Gln	Ala	Ala	His	Leu	Val	Thr	Asp	Asp	Tyr	Ile			
		115					120					125						
Ala	Lys	Tyr	Glu	Glu	Ala	Val	Arg	Arg	Met	Gln	Asp	Leu	Pro	Pro	Asp			
	130					135					140							
Asp	Pro	Arg	Ser	Phe	Met	Gln	Gln	Ala	Asn	Val	His	Arg	Ala	Tyr	Cys			
145					150					155					160			
Asp	Gly																	